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OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/828,217

DATE: 06/08/2001

TIME: 14:47:04

Input Set : C:\PAOLA\09828217.txt

Output Set: N:\CRF3\06082001\I828217.raw

## SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: HIRANO, TOSHIO  
7 KAISHO, TSUNEYASU  
9 (ii) TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING  
10 PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF  
12 (iii) NUMBER OF SEQUENCES: 2  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
16 P.C.  
17 (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
18 (C) CITY: ARLINGTON  
19 (D) STATE: VA  
20 (E) COUNTRY: USA  
21 (F) ZIP: 22202  
23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Floppy disk  
25 (B) COMPUTER: IBM PC compatible  
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
29 (vi) CURRENT APPLICATION DATA:  
C--> 30 (A) APPLICATION NUMBER: US/09/828,217  
C--> 31 (B) FILING DATE: 09-Apr-2001  
32 (C) CLASSIFICATION:  
41 (vii) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: 09/182,563  
36 (B) FILING DATE:  
38 (A) APPLICATION NUMBER: PCT/JP94/01732  
39 (B) FILING DATE: 14-OCT-1994  
42 (A) APPLICATION NUMBER: JP 5-281622  
43 (B) FILING DATE: 15-OCT-1993  
45 (viii) ATTORNEY/AGENT INFORMATION:  
46 (A) NAME: OBLON, NORMAN F.  
47 (B) REGISTRATION NUMBER: 24,618  
48 (C) REFERENCE/DOCKET NUMBER: 7625-001-0 PCT  
50 (ix) TELECOMMUNICATION INFORMATION:  
51 (A) TELEPHONE: 703-413-3000  
52 (B) TELEFAX: 703-413-2220  
55 (2) INFORMATION FOR SEQ ID NO: 1:  
57 (i) SEQUENCE CHARACTERISTICS:  
58 (A) LENGTH: 180 amino acids  
59 (B) TYPE: amino acid  
60 (C) STRANDEDNESS: single  
61 (D) TOPOLOGY: linear  
63 (ii) MOLECULE TYPE: peptide  
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
70 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

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71      1          5          10          15
73      Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
74              20          25          30
76      Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
77              35          40          45
79      Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
80              50          55          60
82      Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
83              65          70          75          80
85      Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
86              85          90          95
88      Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
89              100          105          110
91      Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
92              115          120          125
94      Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
95              130          135          140
97      Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
98              145          150          155          160
100     Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
101              165          170          175
103     Ala Leu Leu Gln
104              180

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## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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121 GTGGAATTCA TGGCATCTAC TTCGTATGAC TATTGCAGAG TGCCCATGGA AGACGGGGGAT      60
123 AAGCGCTGTA AGCTTCTGCT GGGGATAGGA ATTCTGGTGC TCCTGATCAT CGTGATTCTG      120
125 GGGGTGCCCT TGATTATCTT CACCATCAAG GCCAACAGCG AGGCCTGCCG GGACGGCCTT      180
127 CGGGCAGTGA TGGAGTGTCG CAATGTCACC CATCTCCTGC AACAAGAGCT GACCGAGGCC      240
129 CAGAAGGGCT TTCAGGATGT GGAGGCCCAG GCCGCCACCT GCAACCACAC TGTGATGGCC      300
131 CTAATGGCTT CCCTGGATGC AGAGAAGGCC CAAGGACAAA AGAAAGTGGA GGAGCTTGAG      360
133 GGAGAGATCA CTACATTAAA CCATAAGCTT CAGGACGCGT CTGCAGAGGT GGAGCGACTG      420
135 AGAAGAGAAA ACCAGGTCTT AAGCGTGAGA ATCGCGGACA AGAAGTACTA CCCCAGCTCC      480
137 CAGGACTCCA GTCCTGCTGC GCGGCCCCAG CTGCTGATTG TGCTGCTGGG CCTCAGCGCT      540
139 CTGCTGCAGT GAGATCCCAG GAAGCTGGCA CATCTTGGA GGTCCGTCCT GCTCGGCTTT      600
141 TCGCTTGAAC ATTCCCTTGA TCTCATCAGT TCTGAGCGGG TCATGGGGCA ACACGGTTAG      660
143 CGGGGAGAGC ACGGGGTAGC CGGAGAAGGG CCTCTGGAGC AGGTCTGGAG GGGCCATGGG      720
145 GCAGTCCTGG GTGTGGGGAC ACAGTCGGGT TGACCCAGGG CTGTCTCCCT CCAGAGCCTC      780
147 CCTCCGGACA ATGAGTCCCC CCTCTTGCTT CCCACCTGA GATTGGGCAT GGGGTGCGGT      840
149 GTGGGGGGCA TGTGCTGCCT GTTGTATGTT GTTTTTTTT CGGGGGGGGT TGCTTTTTTC      900
151 TGGGGTCTTT GAGCTCCAAA AAATAAACAC TTCCTTTGAG GGAGAGCAAA AAAAAAAAAA      960
153 AAAAAAAAAA AAAAAAAAAA AAAGAATTCC ACCACA                                996

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VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]